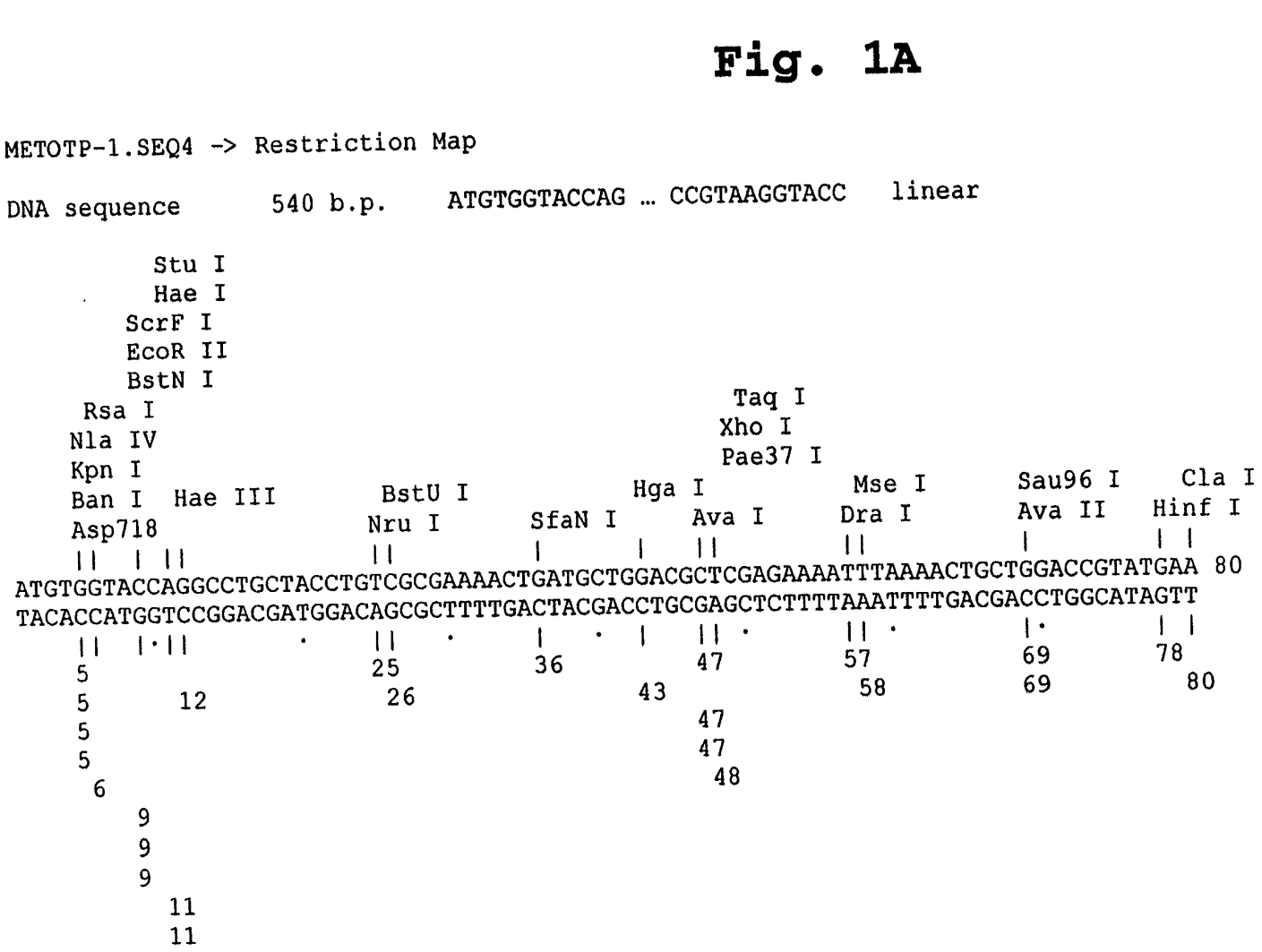
Fig. 1A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Hae I
ScrF I
EcoR II
BstN I
Rsa I
Nla IV
Kpn I
Ban I
Asp718
Hae III
BstU I
Nru I
SfaN I
Hga I
Ava I
Taq I
Xho I
Pae37 I
Mse I
Dra I
Sau96 I
Ava II
Cla I
Hinf I
ATGTGGTACCAGGCCTGCTACCTGTCGCGAAAACTGATGCTGGACGCTCGAGAAAATTTAAAACTGCTGGACCGTATGAA 80
TACACCATGGTCCGGACGATGGACAGCGCTTTTGACTACGACCTGCGAGCTCTTTTAAATTTTGACGACCTGGCATAGTT
5
25
36
47
57
69
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5
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9
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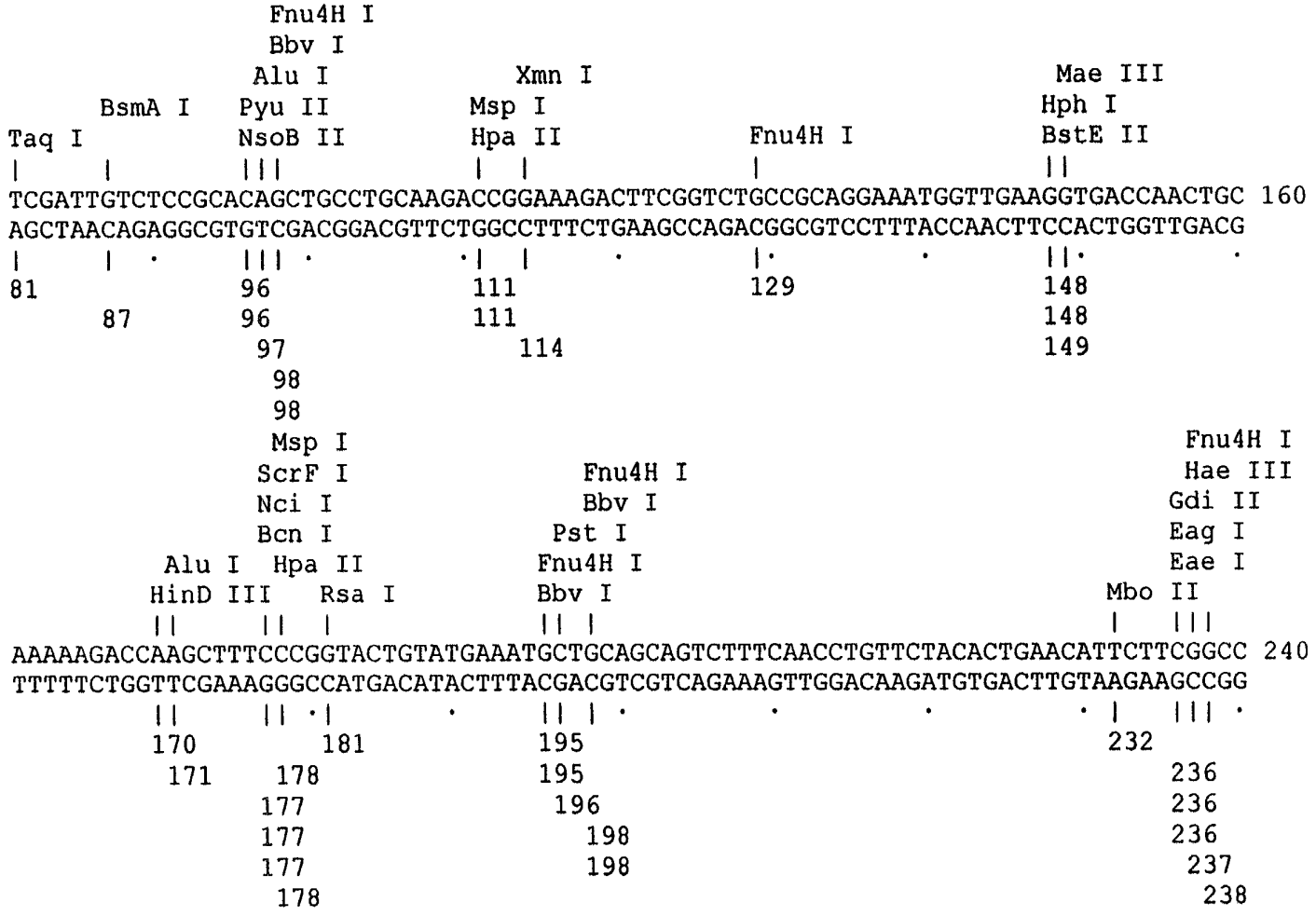
9
11
11

Fig. 1B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Bbv I
Alu I
Xmn I
Mae III
BsmA I
Pyu II
Msp I
Hph I
Taq I
NsoB II
Hpa II
Fnu4H I
BstE II
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148
87
96
111
148
97
114
149
98
98
Msp I
Fnu4H I
Fnu4H I
ScrF I
Hae III
Nci I
Bbv I
Gdi II
Bcn I
Pst I
Eag I
Alu I
Hpa II
Fnu4H I
Eae I
HinD III
Rsa I
Bbv I
Mbo II
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TTTTTCTGGTTCGAAAGGGCCATGACATACTTTACGACGTCGTCAGAAAGTTGGACAAGATGTGACTTGTAAGAAGCCGG
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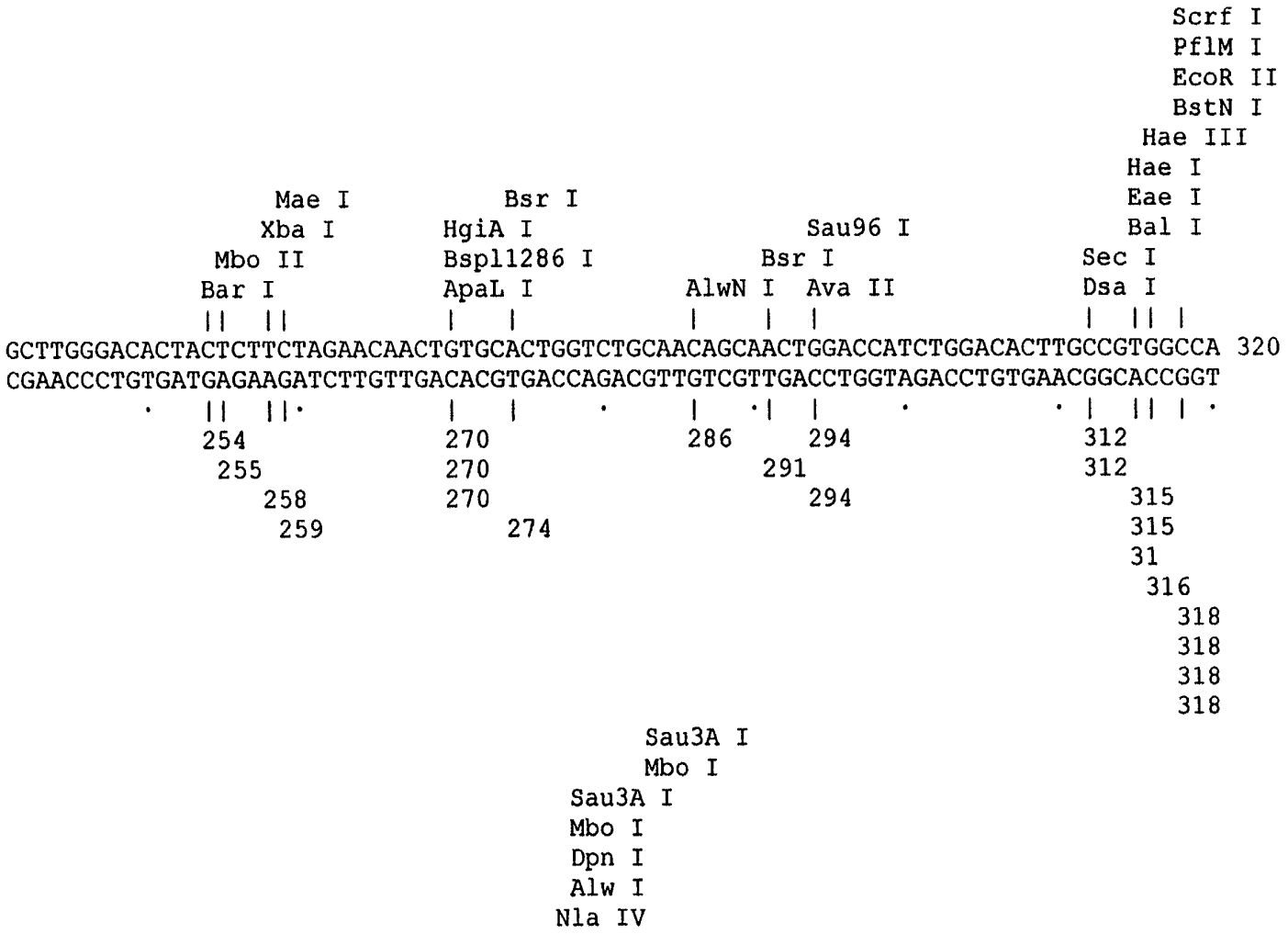
238

Fig. 1C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PflM I
EcoR II
BstN I
Hae III
Hae I
Eae I
Bal I
Sec I
Dsa I
Mae I
Xba I
Mbo II
Bar I
Bsr I
HgiA I
Bspl1286 I
ApaL I
Sau96 I
Bsr I
AlwN I
Ava II
GCTTGGGACACTACTCTTCTAGAACAACTGTGCACTGGTCTGCAACAGCAACTGGACCATCTGGACACTTGCCGTGGCCA 320
CGAACCCTGTGATGAGAAGATCTTGTTGACACGTGACCAGACGTTGTCGTTGACCTGGTAGACCTGTGAACGGCACCGGT
254
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274
286
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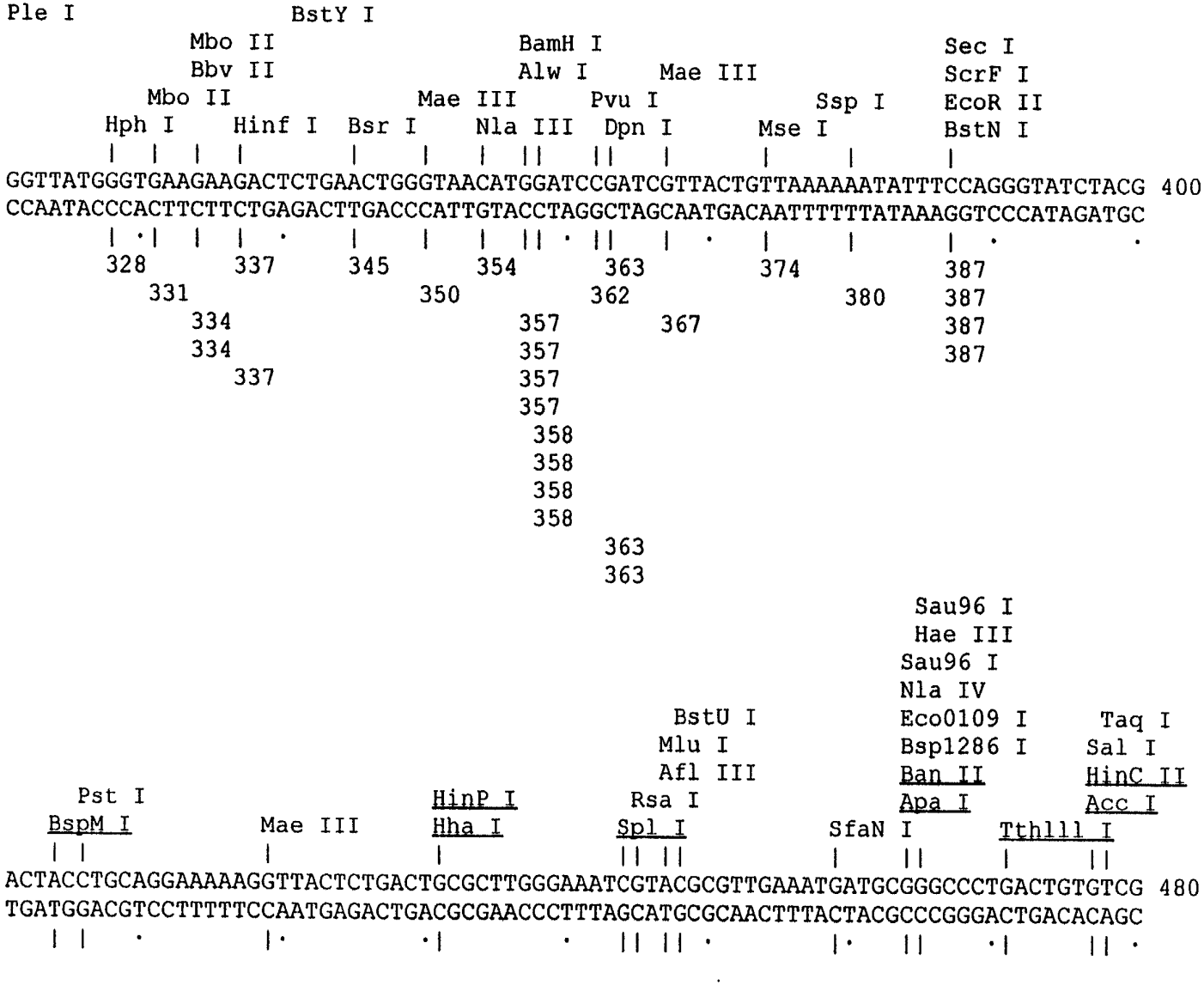
Sau3A I
Mbo I
Sau3A I
Mbo I
Dpn I
Alw I
Nla IV

Fig. 1D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Bbv II
BamH I
Alw I
Mae III
Sec I
ScrF I
Mbo II
Mae III
Pvu I
Ssp I
EcoR II
Hph I
Hinf I
Bsr I
Nla III
Dpn I
Mse I
BstN I
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357
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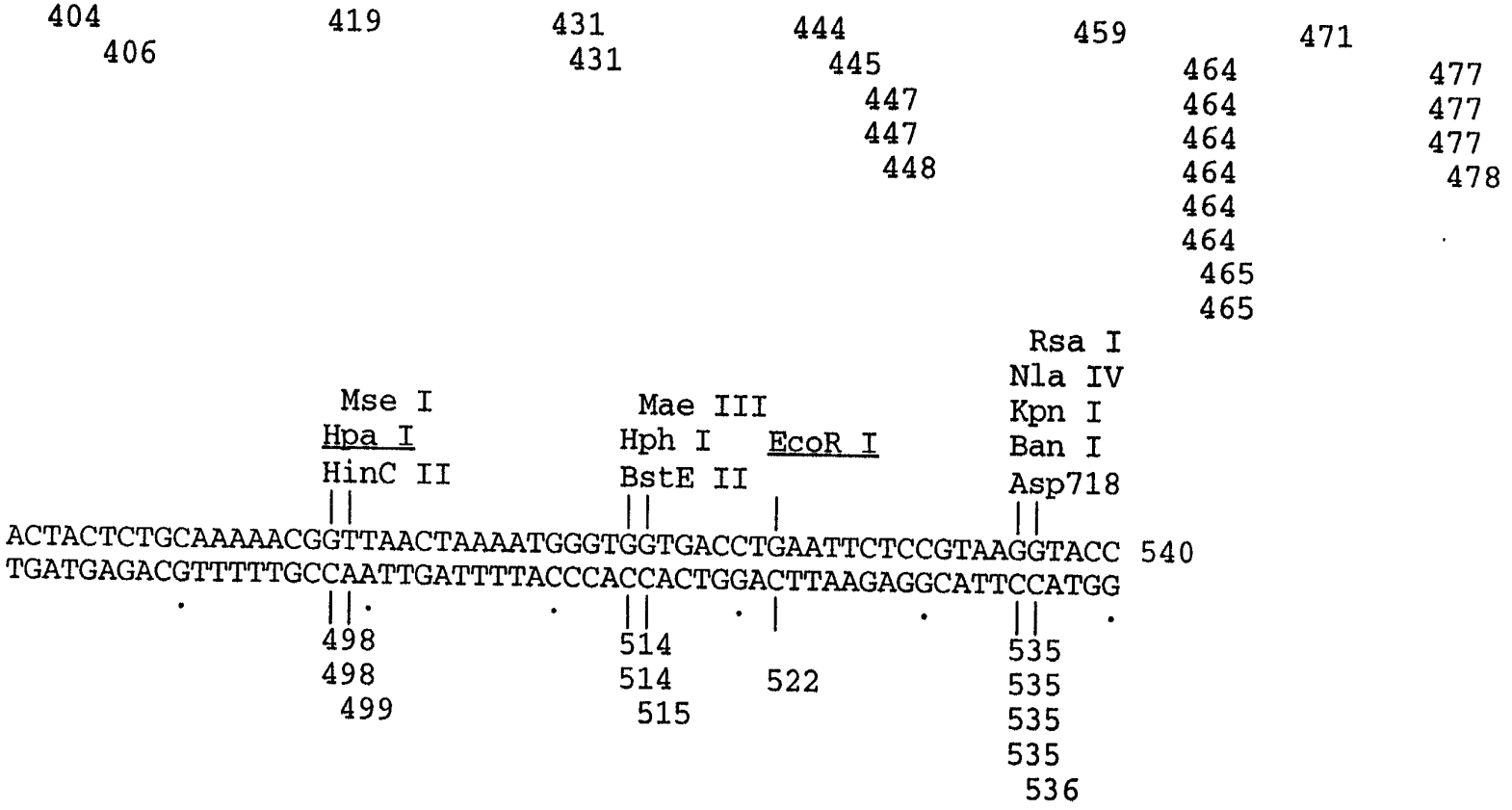
358
358
358
358
363
363
Sau96 I
Hae III
Sau96 I
Nla IV
BstU I
Mlu I
Afl III
Eco0109 I
Bsp1286 I
Ban II
Apa I
Taq I
Sal I
HinC II
Acc I
Pst I
BspM I
Mae III
HinP I
Hha I
Rsa I
Spl I
SfaN I
Tthlll I
ACTACCTGCAGGAAAAAGGTTACTCTGACTGCGCTTGGGAAATCGTACGCGTTGAAATGATGCGGGCCCTGACTGTGTCG 480
TGATGGACGTCCTTTTTCCAATGAGACTGACGCGAACCCTTTAGCATGCGCAACTTTACTACGCCCGGGACTGACACAGC

Fig. 1E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477
477
477
478
Mse I
Hpa I
HinC II
Mae III
Hph I
BstE II
EcoR I
Rsa I
Nla IV
Kpn I
Ban I
Asp718
ACTACTCTGCAAAAACGGTTAACTAAAATGGGTGGTGACCTGAATTCTCCGTAAGGTACC 540
TGATGAGACGTTTTTGCCAATTGATTTTACCCACCACTGGACTTAAGAGGCATTCCATGG
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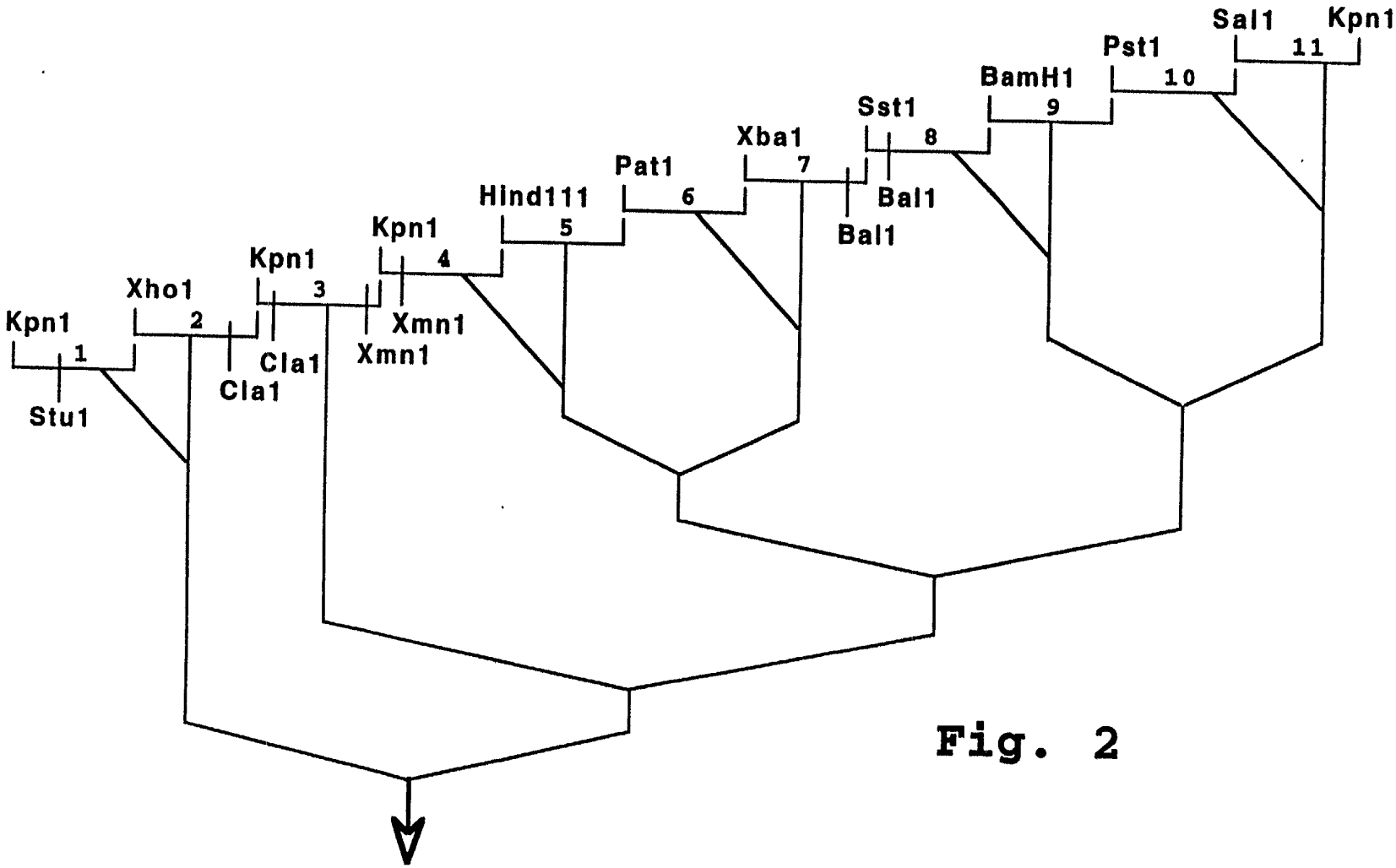

Kpn1
1
Stu1
Xho1
2
Cla1
Kpn1
3
Cla1
Kpn1
4
Xmn1
Xmn1
Hind111
5
Pat1
6
Xba1
7
Sst1
8
Bal1
Bal1
BamH1
9
Pst1
10
Sal1
11
Kpn1

Fig. 2

```
                -23                                                    -9
                met ala phe val leu ser leu leu met ala leu val leu val ser
oIFNt      cccc ATG GCC TTC GTG CTC TCT CTA CTG ATG GCC CTG GTG CTG GTC AGC
htIFN      cccc ATG GCC TTC GTG CTC TCT CTA CTC ATG GCC CTG GTG CTG GTC AGC

-8                              -1  +1                                  11
tyr gly pro gly gly ser leu gly cys tyr leu ser arg lys leu met leu asp ala
TAT GGC CCA GGA GGA TCT CTG GGT TGT TAC CTA TCT CGG AAA CTC ATG CTG GAT GCC
TAC GGC CCA GGA GGA TCC CTG GGT TGT GAC CTG TCT CAG AAC CAC GTG CTG GTT GGC

 12                                  20                                 30
arg glu asn leu lys leu leu asp arg met asn arg leu ser pro his ser cys leu
AGG GAG AAC CTC AAG CTC CTG GAC CGA ATG AAC AGA CTC TCC CCT CAT TCC TGT CTG
AGG AAG AAC CTC AGG CTC CTG GAC GAA ATG AGG AGA CTC TCC CCT CGC TTT TGT CTG

31                                      40                             49
gln asp arg lys asp phe gly leu pro gln glu met val glu gly asp gln leu gln
CAG GAC AGA AAA GAC TTT GGT CTT CCC CAG GAG ATG GTG GAG GGC GAC CAG CTC CAG
CAG GAC AGA AAA GAC TTC GCT TTA CCC CAG GAA ATG GTG GAG GGC GGC CAG CTC CAG

50                                          60                         68
lys asp gln ala phe pro val leu tyr glu met leu gln gln ser phe asn leu phe
AAG GAC CAG GCC TTC CCT GTG CTC TAC GAG ATG CTC CAG CAG AGC TTC AAC CTC TTC
GAG GCC CAG GCC ATC TCT GTG CTC CAT GAG ATG CTC CAG CAG AGC TTC AAC CTC TTC

69   70                                         80                     87
tyr thr glu his ser ser ala ala try asp thr thr leu leu glu gln leu cys thr
TAC ACA GAG CAC TCC TCT GCT GCC TGG GAC ACC ACC CTC CTG GAG CAG CTC TGC ACT
CAC ACA GAG CAC TCC TCT GCT GCC TGG GAC ACC ACC CTC CTG GAG CAG CTC CGC ACT

88       90                                        100                106
gly leu gln gln gln leu asp his leu asp thr cys arg gly gln val met gly glu
GGA CTC CAA CAG CAG CTG GAC CAC CTG GAC ACC TGC AGG GGT CAA GTG ATG GGA GAG
GGA CTC CAT CAG CAG CTG GAC AAC CTG GAT GCC TGC CTG GGG CAG GTG ATG GGA GAG

107         110                                     120                125
glu asp ser glu leu gly asn met asp pro ile val thr val lys lys tyr phe gln
GAA GAC TCT GAA CTG GGT AAC ATG GAC CCC ATT GTG ACC GTG AAG AAG TAC TTC CAG
GAA GAC TCT GCC CTG GGA AGG ACG GGC CCC ACC CTG GCT CTG AAG AGG TAC TTC CAG

126             130                                     140            144
gly ile tyr asp tyr leu gln glu lys gly tyr ser asp cys ala trp glu ile val
GGC ATC TAT GAC TAC CTG CAA GAG AAG GGA TAC AGC GAC TGC GCC TGG GAA ATC GTC
GGC ATC CAT GTC TAC CTG AAA GAG AAG GGA TAC AGC GAC TGC GCC TGG GAA ACC GTC

145                 150                                     160        163
arg val glu met met arg ala leu thr val ser thr thr leu gln lys arg leu thr
AGA GTC GAG ATG ATG AGA GCC CTC ACT GTA TCA ACC ACC TTG CAA AAA AGG TTA ACA
AGA CTG GAA ATC ATG AGA TCC TTC TCT TCA TTA ATC AGC TTG CAA GAA AGG TTA AGA

164                             172
lys met gly gly asp leu asn ser pro end
AAG ATG GGT GGA GAT CTG AAC TCA CCT TGA
ATG ATG GAT GGA GAC CTG AGC TCA CCT TGA
```

Fig. 3

Fig. 4

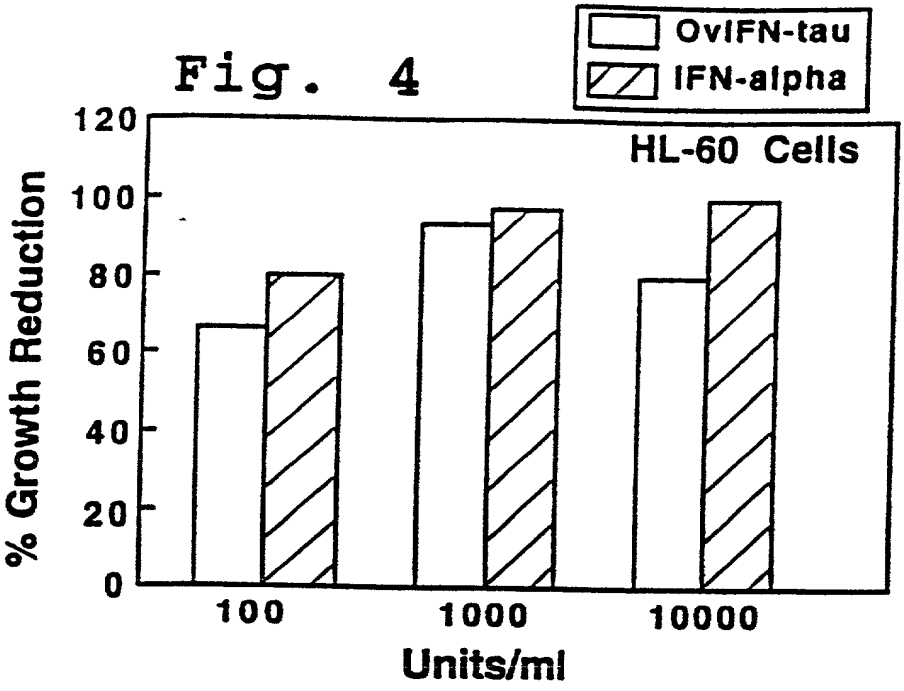
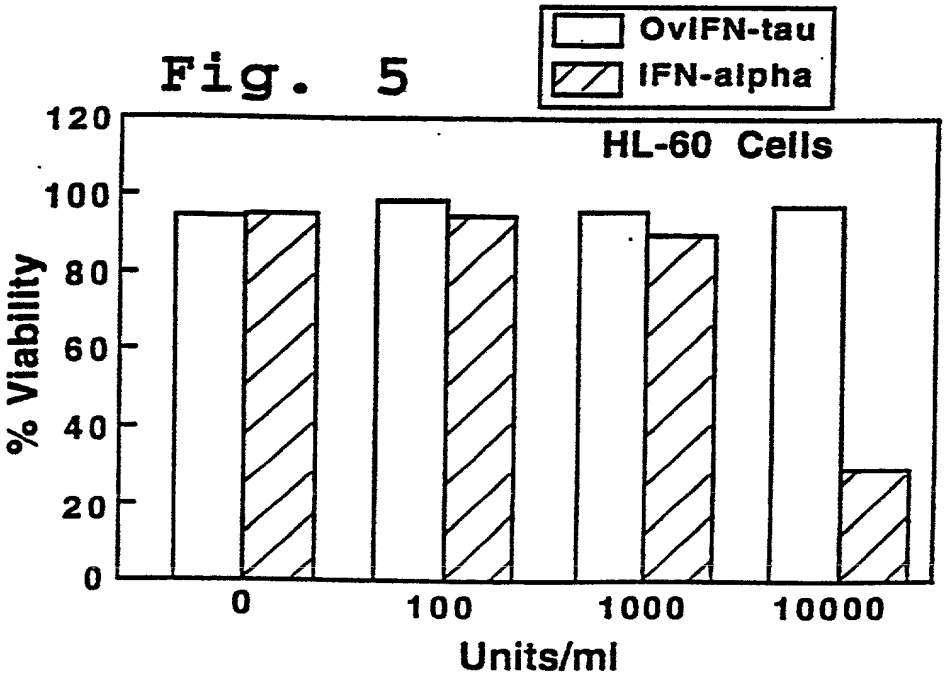

OvIFN-tau
IFN-alpha
HL-60 Cells
% Growth Reduction
120
100
80
60
40
20
0
100
1000
10000
Units/ml

Fig. 5


OvIFN-tau
IFN-alpha
HL-60 Cells
% Viability
120
100
80
60
40
20
0
0
100
1000
10000
Units/ml

Peptides	MW	HI*	Sequence
IFNt(1-37) (SEQ ID NO:5)	4465	-0.78	CYSLRKLMLDARENLKLLDRMNRLSPHSCLQDRKDFG
IFNt(34-64) (SEQ ID NO:6)	3610	-0.72	KDFGLPQEMVEGDQLQKDQAFPVLYEMLQQS
IFNt(62-92) (SEQ ID NO:7)	3586	-0.53	QQSFNLFYTEHSSAAWDTTLLEQLCTGLQQQ
IFNt(90-122) (SEQ ID NO:8)	3712	-0.86	QQQLDHLDTCRGQVMGEEDSELGNMDPIVTVKK
IFNt(119-150) (SEQ ID NO:9)	3948	-0.56	TVKKYFQGIYDYLQEKGYSDCAWEIVRVEMMR
IFNt(139-172) (SEQ ID NO:10)	3818	-0.11	CAWEIVRVEMMRALTVSTTLQKRLTKMGGDLNSP

*Hydropathic Index

Fig. 6

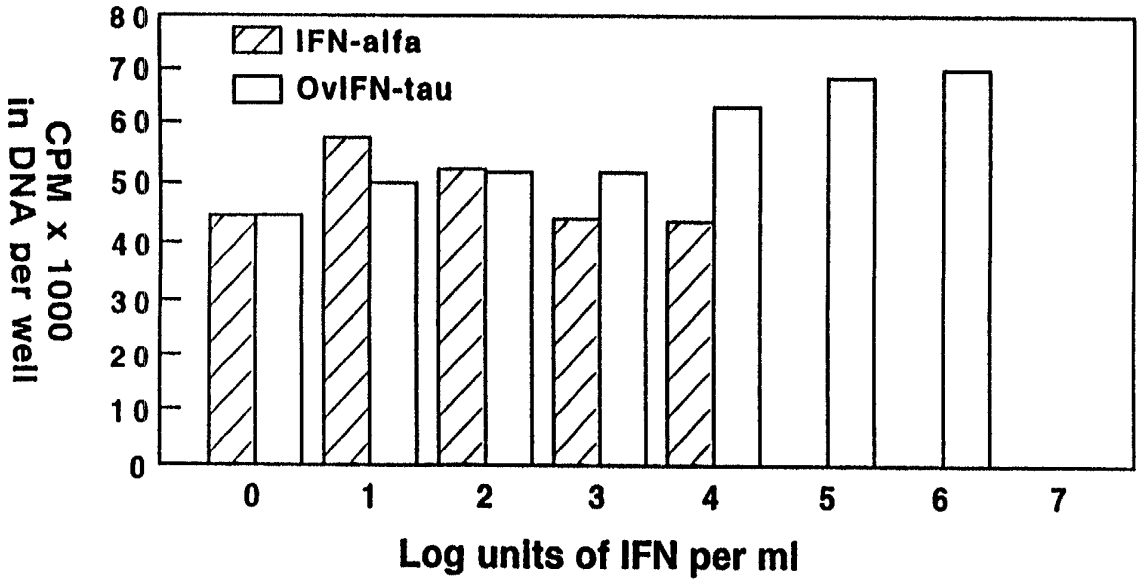
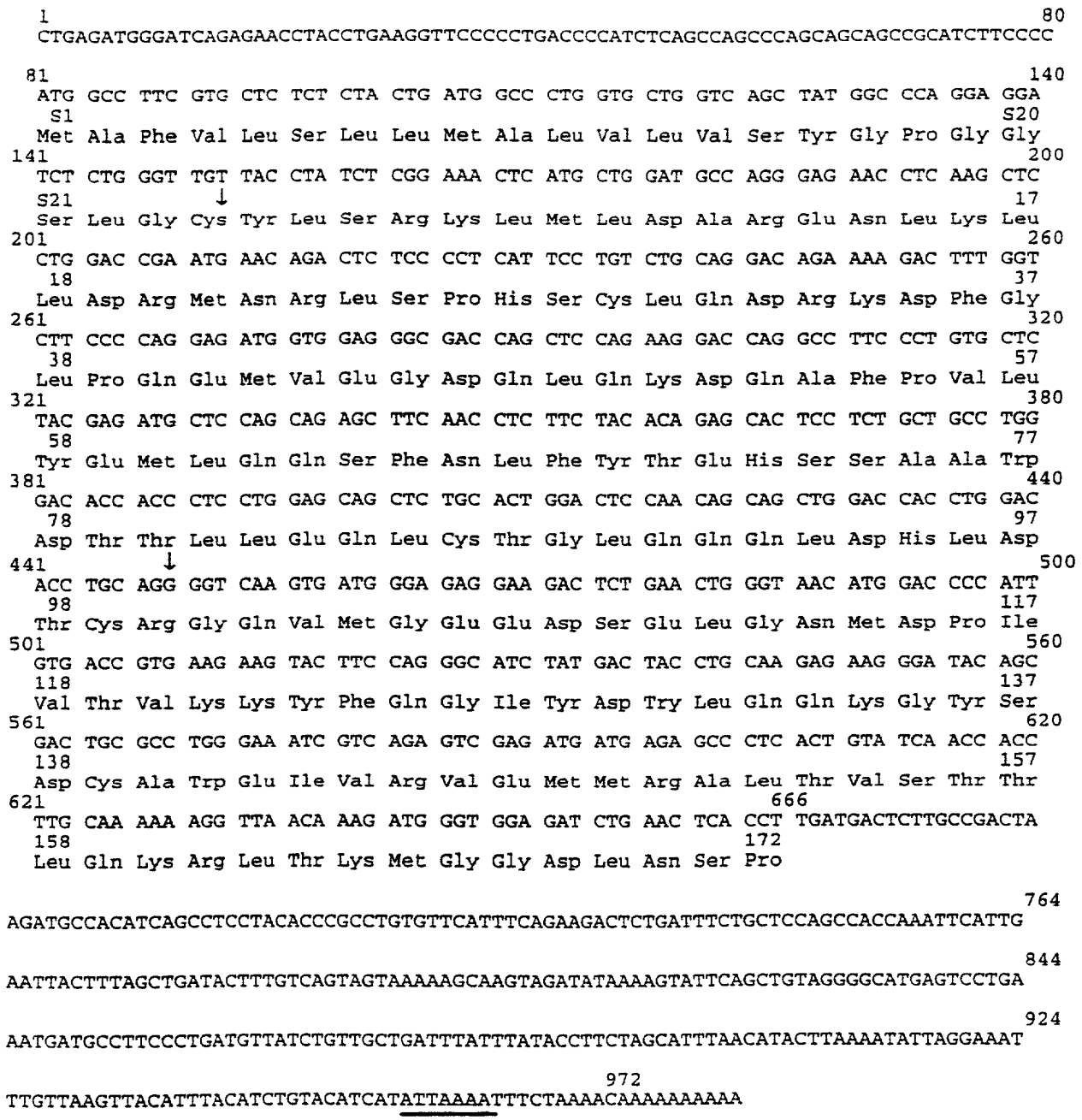


Fig. 8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81
140
ATG GCC TTC GTG CTC TCT CTA CTG ATG GCC CTG GTG CTG GTC AGC TAT GGC CCA GGA GGA
S1
S20
Met Ala Phe Val Leu Ser Leu Leu Met Ala Leu Val Leu Val Ser Tyr Gly Pro Gly Gly
141
200
TCT CTG GGT TGT TAC CTA TCT CGG AAA CTC ATG CTG GAT GCC AGG GAG AAC CTC AAG CTC
S21
17
Ser Leu Gly Cys Tyr Leu Ser Arg Lys Leu Met Leu Asp Ala Arg Glu Asn Leu Lys Leu
201
260
CTG GAC CGA ATG AAC AGA CTC TCC CCT CAT TCC TGT CTG CAG GAC AGA AAA GAC TTT GGT
18
37
Leu Asp Arg Met Asn Arg Leu Ser Pro His Ser Cys Leu Gln Asp Arg Lys Asp Phe Gly
261
320
CTT CCC CAG GAG ATG GTG GAG GGC GAC CAG CTC CAG AAG GAC CAG GCC TTC CCT GTG CTC
38
57
Leu Pro Gln Glu Met Val Glu Gly Asp Gln Leu Gln Lys Asp Gln Ala Phe Pro Val Leu
321
380
TAC GAG ATG CTC CAG CAG AGC TTC AAC CTC TTC TAC ACA GAG CAC TCC TCT GCT GCC TGG
58
77
Tyr Glu Met Leu Gln Gln Ser Phe Asn Leu Phe Tyr Thr Glu His Ser Ser Ala Ala Trp
381
440
GAC ACC ACC CTC CTG GAG CAG CTC TGC ACT GGA CTC CAA CAG CAG CTG GAC CAC CTG GAC
78
97
Asp Thr Thr Leu Leu Glu Gln Leu Cys Thr Gly Leu Gln Gln Gln Leu Asp His Leu Asp
441
500
ACC TGC AGG GGT CAA GTG ATG GGA GAG GAA GAC TCT GAA CTG GGT AAC ATG GAC CCC ATT
98
117
Thr Cys Arg Gly Gln Val Met Gly Glu Glu Asp Ser Glu Leu Gly Asn Met Asp Pro Ile
501
560
GTG ACC GTG AAG AAG TAC TTC CAG GGC ATC TAT GAC TAC CTG CAA GAG AAG GGA TAC AGC
118
137
Val Thr Val Lys Lys Tyr Phe Gln Gly Ile Tyr Asp Try Leu Gln Gln Lys Gly Tyr Ser
561
620
GAC TGC GCC TGG GAA ATC GTC AGA GTC GAG ATG ATG AGA GCC CTC ACT GTA TCA ACC ACC
138
157
Asp Cys Ala Trp Glu Ile Val Arg Val Glu Met Met Arg Ala Leu Thr Val Ser Thr Thr
621
666
TTG CAA AAA AGG TTA ACA AAG ATG GGT GGA GAT CTG AAC TCA CCT TGATGACTCTTGCCGACTA
158
172
Leu Gln Lys Arg Leu Thr Lys Met Gly Gly Asp Leu Asn Ser Pro
764
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844
AATTACTTTAGCTGATACTTTGTCAGTAGTAAAAAGCAAGTAGATATAAAAGTATTCAGCTGTAGGGGCATGAGTCCTGA
924
AATGATGCCTTCCCTGATGTTATCTGTTGCTGATTTATTTATACCTTCTAGCATTTAACATACTTAAAATATTAGGAAAT
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Fig. 7

Fig. 9

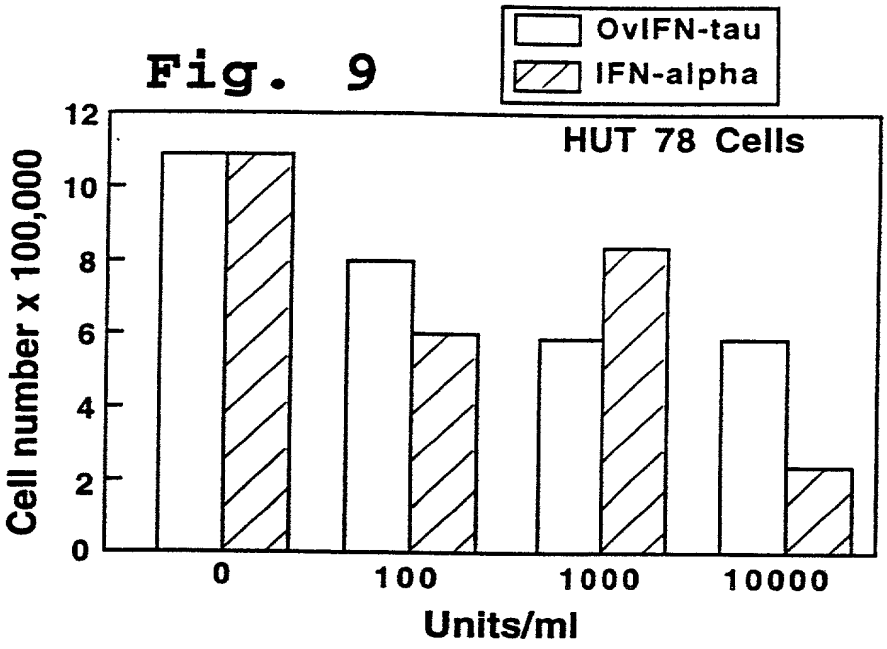

OvIFN-tau
IFN-alpha
HUT 78 Cells
Cell number x 100,000
0
2
4
6
8
10
12
0
100
1000
10000
Units/ml

Fig. 10

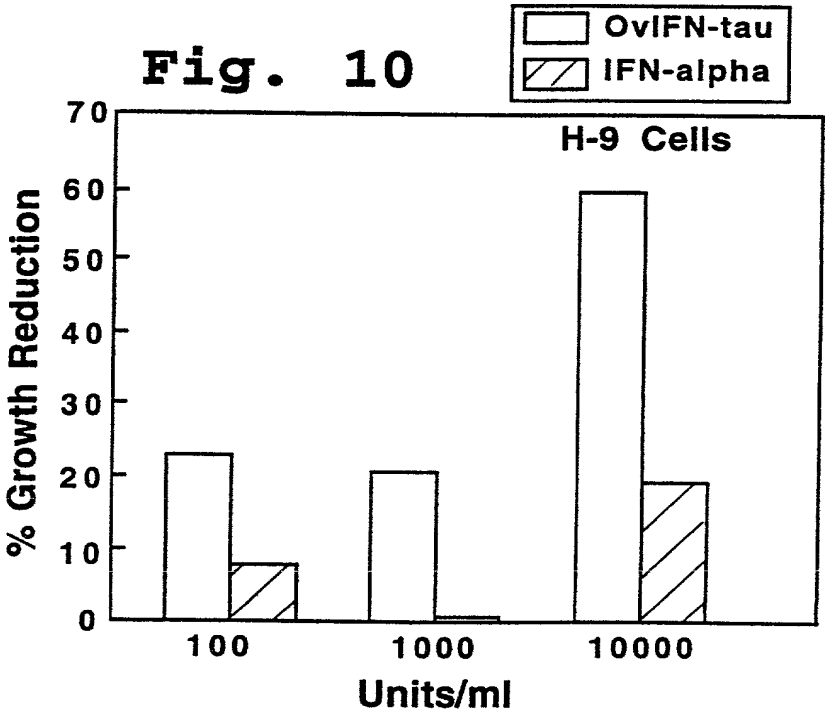

OvIFN-tau
IFN-alpha
H-9 Cells
% Growth Reduction
0
10
20
30
40
50
60
70
100
1000
10000
Units/ml

Fig. 11A

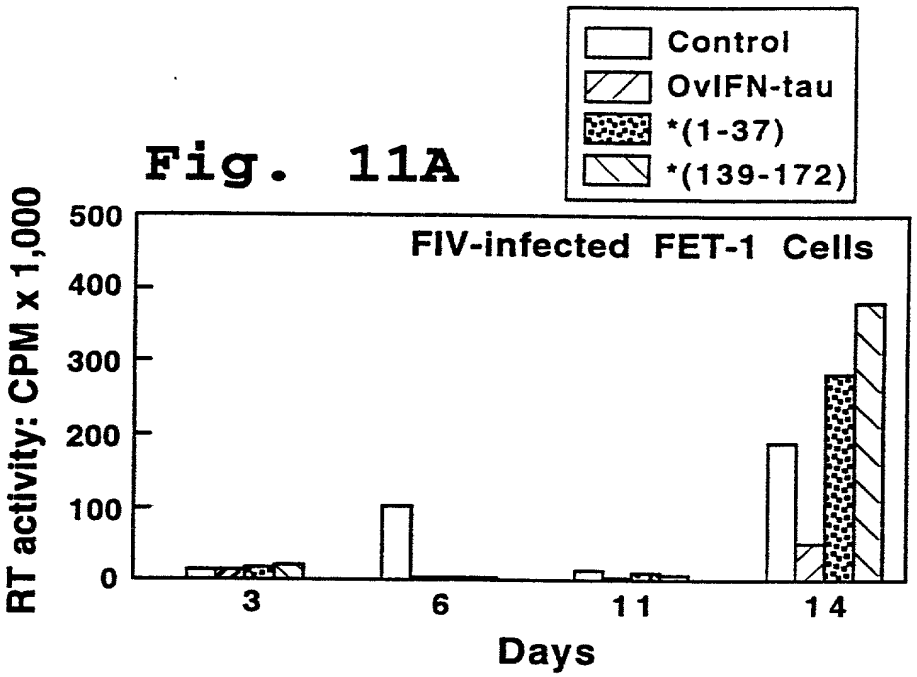


Fig. 11B

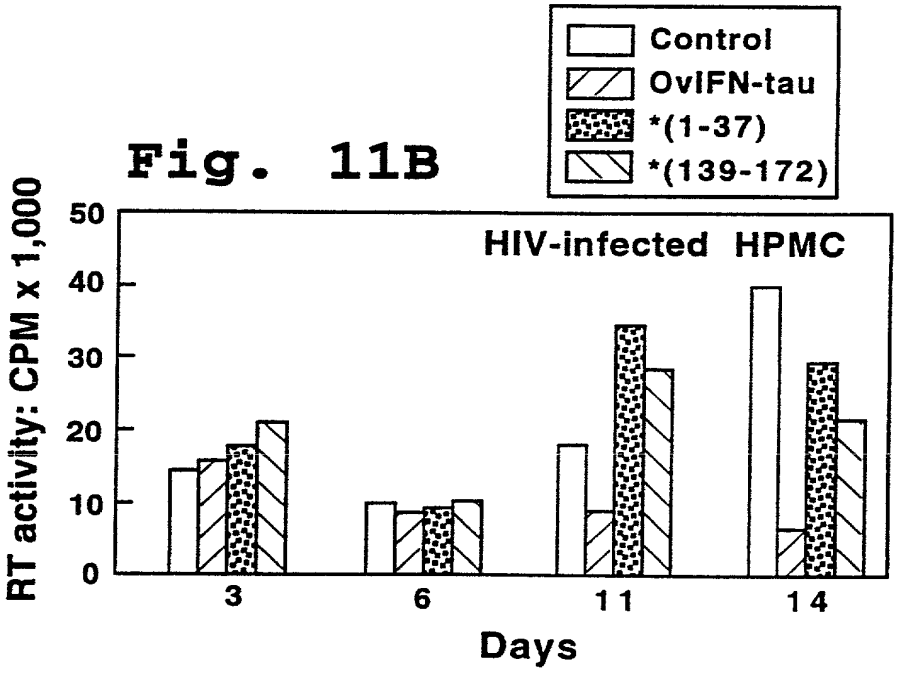


Fig. 12

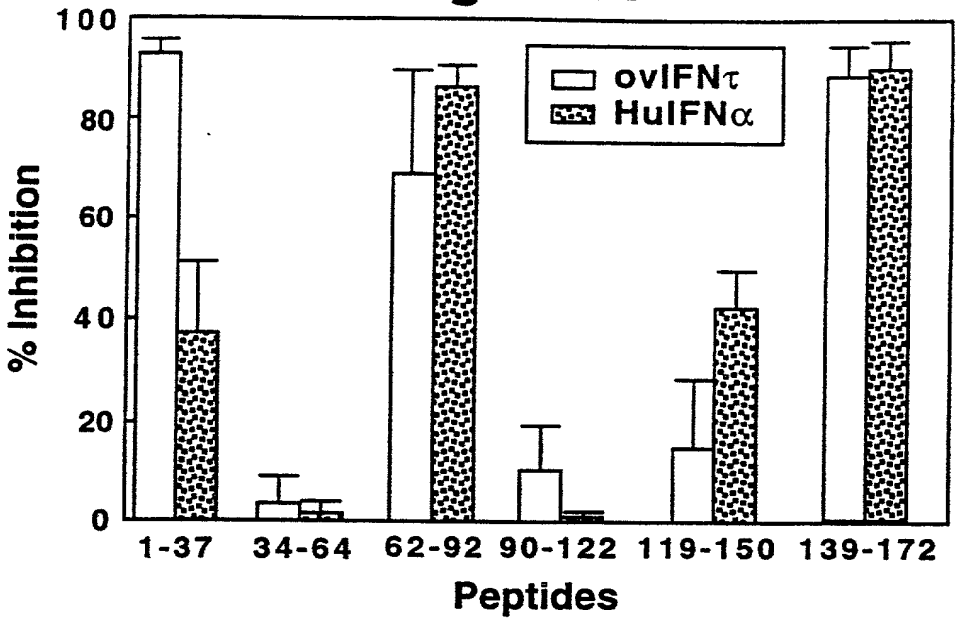

100
80
60
40
20
0
% Inhibition
ovIFNτ
HuIFNα
1-37
34-64
62-92
90-122
119-150
139-172
Peptides

Fig. 13

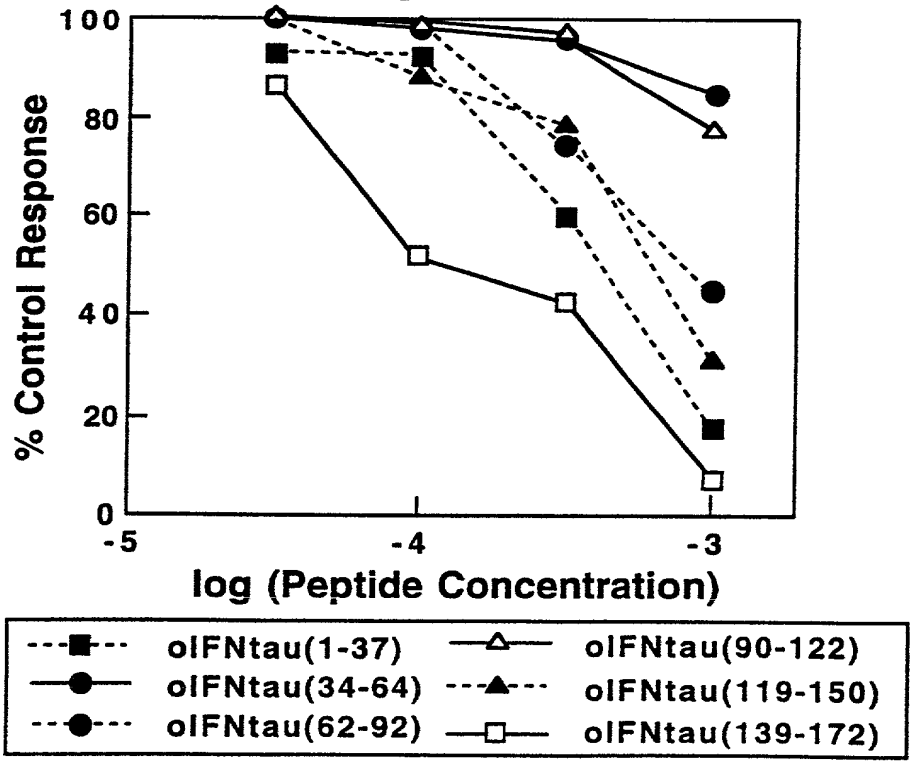
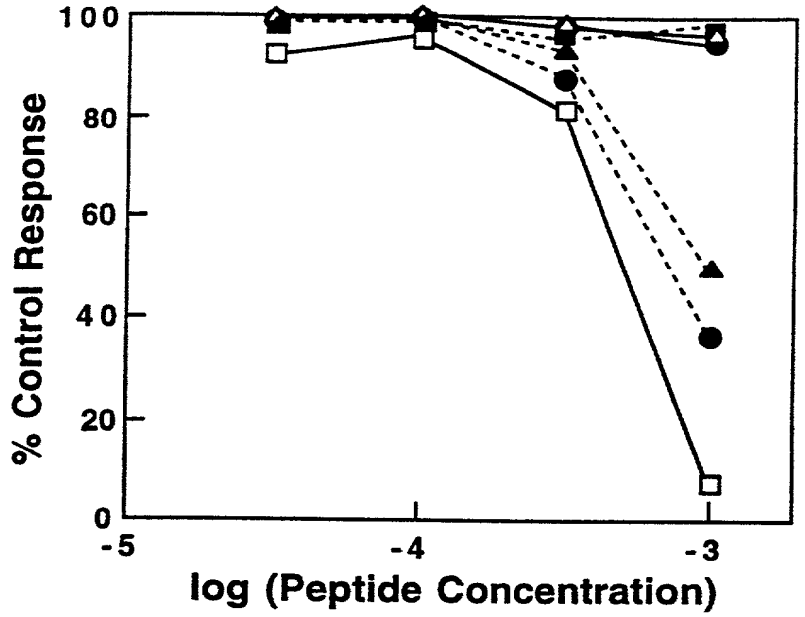

100
80
60
40
20
0
% Control Response
-5
-4
-3
log (Peptide Concentration)
oIFNtau(1-37)
oIFNtau(34-64)
oIFNtau(62-92)
oIFNtau(90-122)
oIFNtau(119-150)
oIFNtau(139-172)

Fig. 14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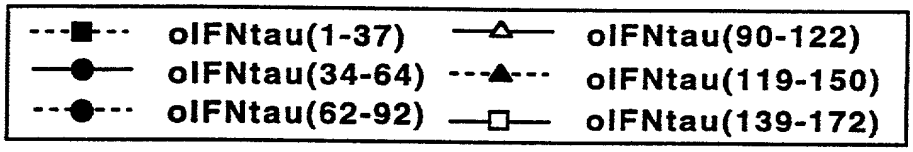
80
60
40
20
0
% Control Response
-5
-4
-3
log (Peptide Concentration)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oIFNtau(34-64)
oIFNtau(62-92)
oIFNtau(90-122)
oIFNtau(119-150)
oIFNtau(139-172)

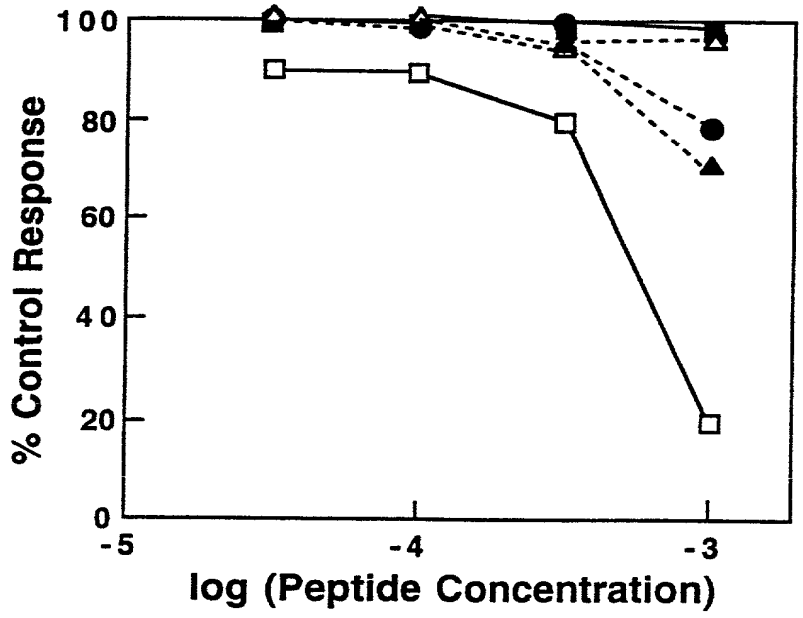

100
80
60
40
20
0
% Control Response
-5
-4
-3
log (Peptide Concentration)

Fig. 15

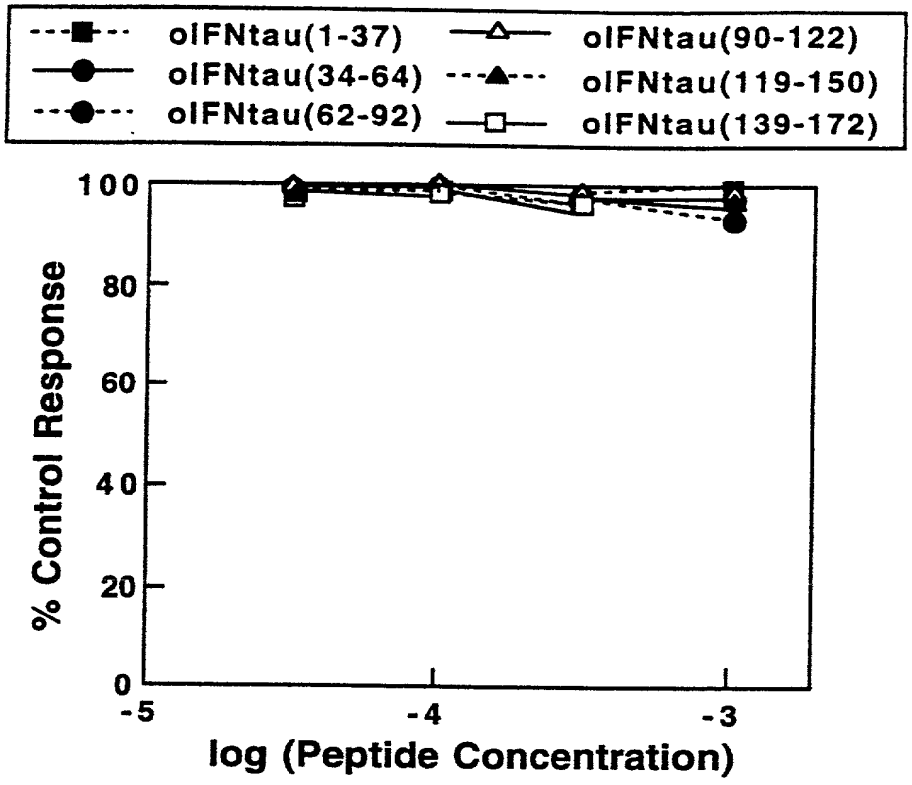
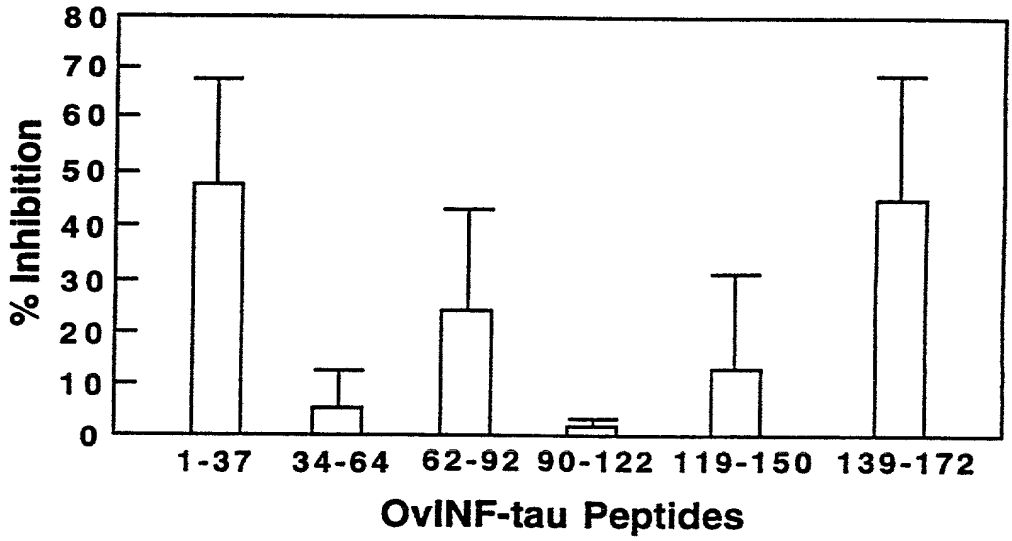

olFNtau(1-37)
olFNtau(34-64)
olFNtau(62-92)
olFNtau(90-122)
olFNtau(119-150)
olFNtau(139-172)
% Control Response
100
80
60
40
20
0
-5
-4
-3
log (Peptide Concentration)

Fig. 16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80
70
60
50
40
30
20
10
0
1-37
34-64
62-92
90-122
119-150
139-172
OvINF-tau Peptides

Fig. 17

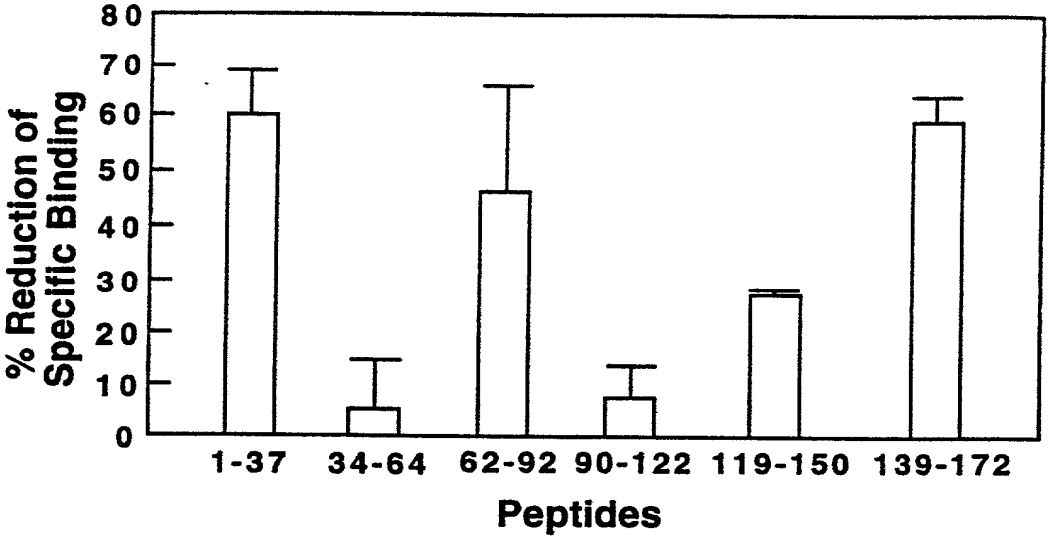
% Reduction of Specific Binding
80
70
60
50
40
30
20
10
0
1-37
34-64
62-92
90-122
119-150
139-172
Peptides

Fig. 18

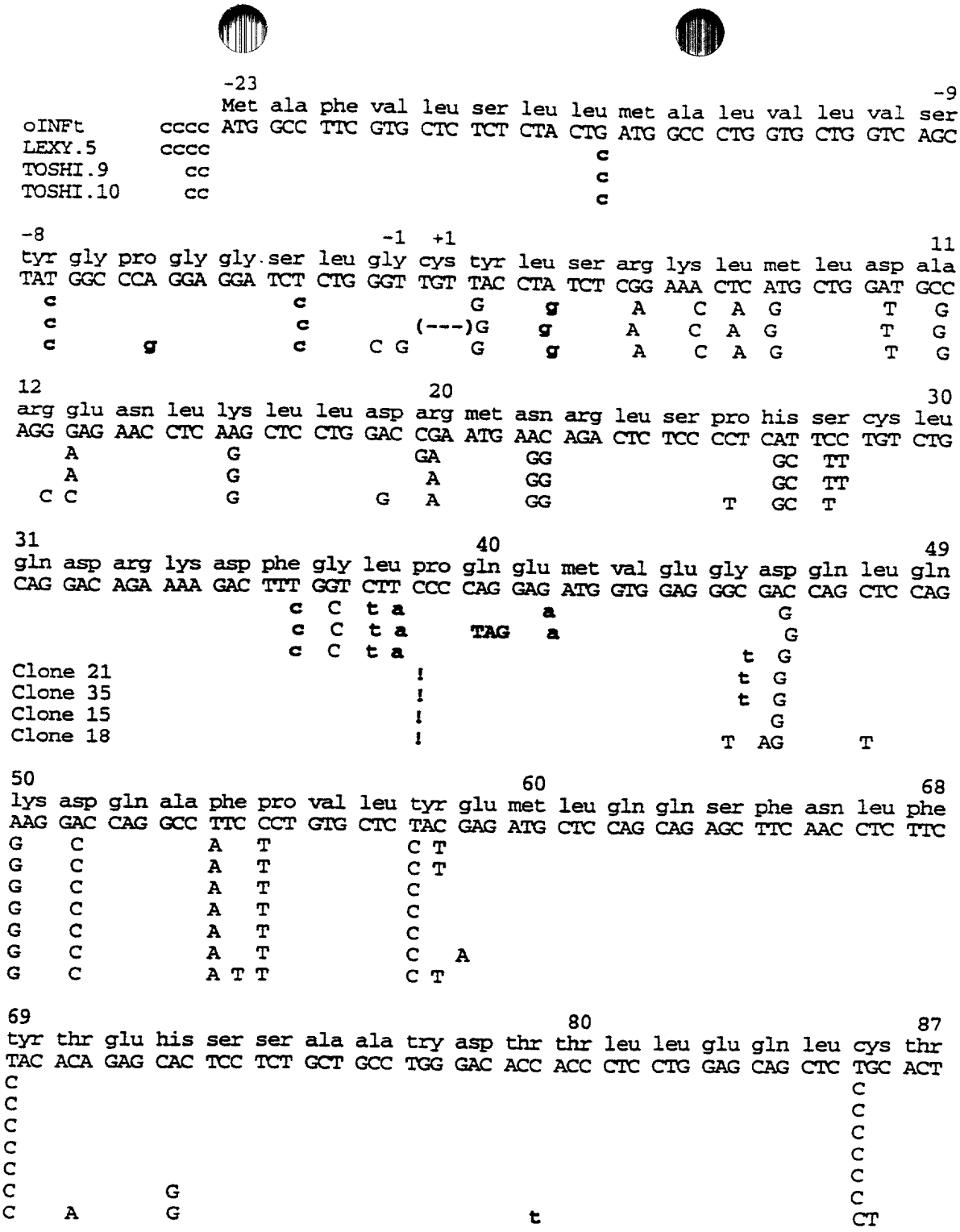
-23 -9
Met ala phe val leu ser leu leu met ala leu val leu val ser
oINFt cccc ATG GCC TTC GTG CTC TCT CTA CTG ATG GCC CTG GTG CTG GTC AGC
LEXY.5 cccc
TOSHI.9 cc
TOSHI.10 cc
-8 -1 +1 11
tyr gly pro gly gly ser leu gly cys tyr leu ser arg lys leu met leu asp ala
TAT GGC CCA GGA GGA TCT CTG GGT TGT TAC CTA TCT CGG AAA CTC ATG CTG GAT GCC
12 20 30
arg glu asn leu lys leu leu asp arg met asn arg leu ser pro his ser cys leu
AGG GAG AAC CTC AAG CTC CTG GAC CGA ATG AAC AGA CTC TCC CCT CAT TCC TGT CTG
31 40 49
gln asp arg lys asp phe gly leu pro gln glu met val glu gly asp gln leu gln
CAG GAC AGA AAA GAC TTT GGT CTT CCC CAG GAG ATG GTG GAG GGC GAC CAG CTC CAG
Clone 21
Clone 35
Clone 15
Clone 18
50 60 68
lys asp gln ala phe pro val leu tyr glu met leu gln gln ser phe asn leu phe
AAG GAC CAG GCC TTC CCT GTG CTC TAC GAG ATG CTC CAG CAG AGC TTC AAC CTC TTC
69 80 87
tyr thr glu his ser ser ala ala try asp thr thr leu leu glu gln leu cys thr
TAC ACA GAG CAC TCC TCT GCT GCC TGG GAC ACC ACC CTC CTG GAG CAG CTC TGC ACT

Fig. 19A

```
88      90                                      100                     106
gly leu gln gln gln leu asp his leu asp thr cys arg gly gln val met gly glu
GGA CTC CAA CAG CAG CTG GAC CAC CTG GAC ACC TGC AGG GGT CAA GTG ATG GGA GAG
          T                 A         t G       CT    g   g
          T                 A         t G       CT    g   g
          T               t G         t G       CT    g   g      C
          T               t G         t G       CT    g   g      C
          T               t G         t G       CT    g   g      C
          T               t G           G       CT    g   g      C
          T               t G         t G     t CT    g   g T    CT

107         110                                     120                 125
glu asp ser glu leu gly asn met asp pro ile val thr val lys lys tyr phe gln
GAA GAC TCT GAA CTG GGT AAC ATG GAC CCC ATT GTG ACC GTG AAG AAG TAC TTC CAG
             CC       a  GG  C   G       CC C   G T C            G
             CC       a  GG  C   G       CC C   G T C            G
             CC       a  GA  C   G       CC C   G   A            G    t
             CC       a  GG  C   G       CC C   G   A            C    t
             CC       a  GG  C   G       CC C   G   A            C    t
             CC       a  GG  C   G       CC C   G                GC
             CC       a  GG  C   G       CC C   G                GC

126             130                                     140             144
gly ile tyr asp tyr leu gln glu lys gly tyr ser asp cys ala trp glu ile val
GGC ATC TAT GAC TAC CTG CAA GAG AAG GGA TAC AGC GAC TGC GCC TGG GAA ATC GTC
        C    T          A                                            C
        C    T          A                                            C
        C    T          A                 t   t                       t
        C    T          A                 t   t                 !
        C    T          A                 t   !
        C   AT                                         !
        C    T                        !

145                 150                                     160         163
arg val glu met met arg ala leu thr val ser thr thr leu gln lys arg leu thr
AGA GTC GAG ATG ATG AGA GCC CTC ACT GTA TCA ACC ACC TTG CAA AAA AGG TTA ACA
    C G   a   C         T   T   T   TC   T   T   G          G            G
      g   a   C         T   T   T   TC   T   T   G          G            G
    C G   a   C         T   t g T   TC           G        C              G

164                             172
lys met gly gly asp leu asn ser pro
AAG ATG GGT GGA GAT CTG AAC TCA CCT TGA
 T       A        c      G
 T       A        c      G
 T       A        c      G
```

Fig. 19B

```
                -23                                                    -9
oTP-1           Met ala phe val leu ser leu leu met ala leu val leu val ser
LEXY.5
TOSHI.9
TOSHI.10

-8                              -1  +1                                  11
tyr gly pro gly gly ser leu gly cys tyr leu ser arg lys leu met leu asp ala
                                    asp         gln asn his val     val gly
                               (---)asp         gln asn his val     val gly
                              arg   asp         gln asn his val     val gly

12                                  20                                  30
arg glu asn leu lys leu leu asp arg met asn arg leu ser pro his ser cys leu
    lys         arg             glu     arg                 arg phe
    lys         arg             gln     arg                 arg phe
ser gln         arg         gly gln     arg             leu arg phe

31                                      40                          49
gln asp arg lys asp phe gly leu pro gln glu met val glu gly asp gln leu gln
                        ala                                 gly
                        ala         (Stop)                   gly
                        ala                                 gly
Clone 21                            !                           gly
Clone 35                        !                           gly
Clone 15                        !                           gly
Clone 18                        !                   val ser     phe

50                                      60                          68
lys asp gln ala phe pro val leu tyr glu met leu gln gln ser phe asn leu phe
glu ala         ile ser         his
glu ala         ile ser         his
glu ala         ile ser         his
glu ala         ile ser         his
glu ala         ile ser         his
glu ala         ile ser         his lys
glu ala         ile ser         his

69                                              80                  87
tyr thr glu his ser ser ala ala try asp thr thr leu leu glu gln leu cys thr
his                                                                 arg
his                                                                 arg
his                                                                 arg
his                                                                 arg
his                                                                 arg
his         arg                                                     arg
his lys     arg                                                     leu
```

Fig. 20A

88	90								100					106
gly	leu	gln	gln	gln	leu	asp	his	leu	asp	thr	cys	arg	gly	gln	val	met	gly	glu
		his					asn			ala		leu						
		his					asn			ala		leu						
		his					asp			ala		leu				thr		
		his					asp			ala		leu				thr		
		his					asp			ala		leu				thr		
		his					asp			ala		leu				thr		
		his					asp			ala		leu			leu	thr		

107		110									120					125
glu	asp	ser	glu	leu	gly	asn	met	asp	pro	ile	val	thr	val	lys	lys	tyr	phe	gln
			ala			arg	thr	gly		thr	leu	ala	leu		arg			
			ala			arg	thr	gly		thr	leu	ala	leu		arg			
			ala			arg	thr	gly		thr	leu	ala	met		arg			
			ala			arg	thr	gly		thr	leu	ala	met		thr			
			ala			arg	thr	gly		thr	leu	ala	met		thr			
			ala			arg	thr	gly		thr	leu	ala			ser			
			ala			arg	thr	gly		thr	leu	ala			ser			

126			130									140				144
gly	ile	tyr	asp	tyr	leu	gln	glu	lys	gly	tyr	ser	asp	cys	ala	trp	glu	ile	val
		his	val			lys										thr		
		his	val			lys										thr		
		his	val			lys												
		his	val			lys												
		his	val			lys												
		his	ile															
		his	val															

145				150									160			163
arg	val	glu	met	met	arg	ala	leu	thr	val	ser	thr	thr	leu	gln	lys	arg	leu	thr
	leu		ile		ser	phe	ser	ser	leu	ile	ser			glu				arg
			ile		ser	phe	ser	ser	leu	ile	ser			glu				arg
	leu		ile		ser		ser	ser			ser		his					arg

164						172	
lys	met	gly	gly	asp	leu	asn	ser	pro	**stop**
met		asp				ser			**stop**
met		asp				ser			**stop**
met		asp				ser			**stop**

Fig. 20B

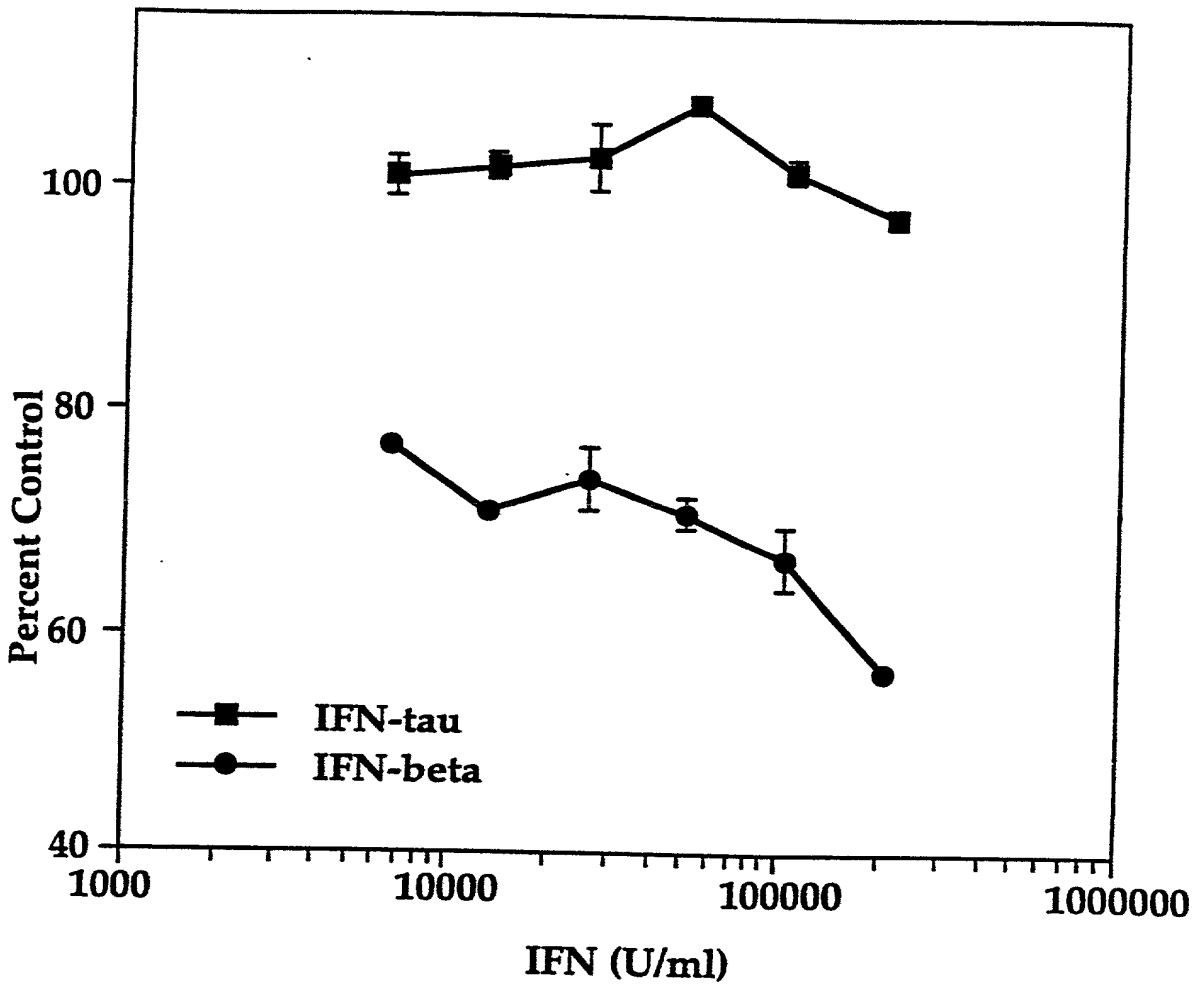
100
80
60
40
Percent Control
1000
10000
100000
1000000
IFN (U/ml)
IFN-tau
IFN-beta

Fig. 21